

A. FIGURE 1: FIGURE 1

SEQ ID NO:1:

GGCATATTAGCTTGGGTTACTGTGAATTCTGACAGGTCAAGCTGCATGCCACAGA  
 CAGGAGACTGTGGGGACCTTGGACCTAGGGGGAGCCTCCACCCAAATCACGTTCT  
 GCCCCAGTTGAGAAAACCTCTGGAACAAACTCCTAGGGGCTACCTCACTTCTTGA  
 GATGTTAACAGCACTATAAGCTCTACACATAGTTACCTGGGATTGGATTGAA  
 AGCTGCAAGACTAGCAACCCTGGAGCCCTGGAGACAGAAGGGACTGATGGGCACA  
 CTTCCGGAGTGCCTGT

SEQ ID NO:2:

GCGGGCTGCCCGCGCAAGGGTGGCGCGCGCGTTTCTTGTTCCTGGTCAACAAAG  
 AAATGTGGAGTGTCTGGCTGAATCCTCATACAGACAAGATCATTATGGTGCTGTTA  
 GGTTGAAAAAGTGATATAATAAAGGAACCAAGGAGAAAATTAGAAGGAAAGAAA  
 AAATTGCCTCTGCAGGTGTGCGAGCAGGATTGCTTCTGCAACAAAAGCCTCCACCCA  
 GCCACATCTTGGGAAAAGAATGGCCTTCTGGGACAGTCTTCAATGCTG  
 GGTATCCTGTGTTGCAGCGCTGTCTCCCACAGGAACCAGCAGACTTGGTTGAGGG  
 TATCTTCCTGTCATGCCATGTGCCCCATCAATGTCAGCGCCAGCACCTGTATGGAATT  
 ATGTTGATGCAAGGAGCACTGGAACTCGAATTCAATGTTACACCTTGTGCAGAAA  
 ATGCCAGGACAGCTTCCAATTCTAGAAGGGGAAGTCTTGTGATTCTGTGAAGCCAGGA  
 CTTCCTGCTTGTAGATCAACCTAACGAGGTGCTGAGACCCTCAAGGGCTCTTA  
 GAGGTGGCAAAGACTCAATCCCCGAAGTCACTGGAAAAAGACCCAGTGGCCT  
 AAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCAAGGCTCTGCTCT  
 TTGAGGTAAGGGAGATCTTCAGGAAGTCACCTTCTGGTACCAAGGGCAGTGT  
 GCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGTTACTGTGAATTCTGA  
 CAGGTCAAGCTGCATGCCACAGACAGGAGACTGTGGGACCTGGACCTAGGGGA  
 GCCTCCACCCAAATCACGTTCTGCCAGTTGAGAAAACCTGGAACAAACTCCT  
 AGGGGCTACCTCACTTCCTTGAGATGTTAACAGCACTTATAAGCTCTACACAT  
 AGTACCTGGATTGGAAAGCTGCAAGACTAGCAACCCCTGGAGCCCTGGA  
 GACAGAAGGGACTGATGGGACACTTCCGGAGTGCCTGTTACCGAGATGGTGG  
 AAGCAGAGTGGATCTTGGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAAGGG  
 GAGGTGGGCTTGAGCCCTGCTATGCCGAAGTGCTGAGGGTGGTACGAGGAAA  
 ACTTCACCCAGAGGGAGGTCCAGAGAGGTTCTATGCTTCTTACTATTATGA  
 CCGAGCTGTTGACACAGACATGATTGATTATGAAAAGGGGGTATTAAAAGTTGA  
 AGATTGAAAGAAAAGCCAGGGAAAGTGTGATAACTGGAAAACCTCACCTCAG  
 GCAGTCCTTCTGTGCATGGATCTCAGCTACATCACAGCCCTGTTAAAGGATGGCT  
 TTGGCTTGCAGACAGCACAGTCTTACAGCTCACAAAGAAAAGTGAACAAACATAGAG  
 ACGGGCTGGGCCTGGGGGCCACCTTCACTGTTGCAGTCTCTGGCATCTCCAT  
 TGAGGCCACGTACTTCCTGGAGACCTGCATTGCCAACACCTTTAAGGGGAGGA  
 GAGAGCACTTAGTTCTGAACTAGTCTGGGACATCCTGGACTTGAGCCTAGAGATT  
 WRGTTAATTAASCGGCCGAGCTTATCCTTWATRAGGTAATTACTTGCMTGGCCGCG  
 TTTACACGTCGTGATGGNAAACCTGCGTCCAACTAACGCTTGAASAMATCCCCTCG  
 CAGCTGCGATAACAAAAGCCGACGACGCCACAGTGCCA

Figure 1

Atty Docket No. 28110/35908

Serial No.: 09/370,265

Title: Methods and Materials Relating to Novel  
CD39-Like Polypeptides

Figure 2

SEQ ID NO:3.

MATSWGTVFMLVVSCVCSAVSHRNQQTWFEGIFLSSMCPINVASTLYGIMFDAGSTG  
TRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSH  
WKKTPVVLKATAGLRLPEHKAKALLFEVKEIFRKSPFLVPKGSVSIMDGSDLEGILAWV  
TVNFLTGQLHGHRQETVGTLGGASTQITFLPQFEKTLEQTPRGYLTSEMNSTYKLY  
THSYLGFLKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEG  
EVGFEP CYAEVLRVVVRGKLHQPEEVQRGSFYAFSYYYDRAVDTDMIDYEKGGLKVED  
FERKAREVCDNLENFTSGSPFLCMDLSYTALLKDGFGFADSTVLQLTKKVNNIETGWA  
LGATFHLLQSLGISH

Figure 2

**Figure 3**

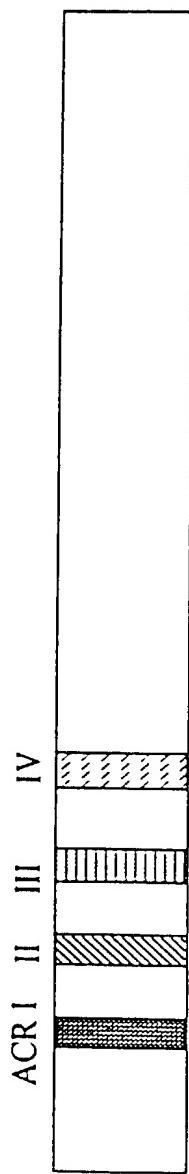
Figure 3

**Figure 4**

|     |   |     |           |
|-----|---|-----|-----------|
| 1   | MATSWGTUFFMLVVSCVCSAUSHRNQCTWFEQIFJGSMCP        | 246 | prot      |
| 1   | MATSWGAVFIMIAACVGSSTVFPYRQCTWFEQIFJGSMCP        | 246 | mut npase |
| 41  | ENVSASLTYGIMFDAGSTGTRIHVYTFTVQKAMPQQLPFILEG     | 246 | prot      |
| 40  | ENVSACTFYGIMFDAGSTGTRIHVYTFTVQKTAQQLPFILEG      | 246 | mut npase |
| 81  | EVFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSFW        | 246 | prot      |
| 80  | EEDDSVKPGLSAFVEQPKQGAETVQIEELLEVAKDSIPRSFW      | 246 | mut npase |
| 121 | KIKTPPVVLKATAGLRLLPKHKAALKALIEIEVK'EIFRKNSPFLVP | 246 | prot      |
| 120 | EITPPVVLKATAGLRLLPQKACALLEVEEIEKNSPFLVP         | 246 | mut npase |
| 161 | KIGSVSIMDGSDLEGILAWVTVNFLTGTQLHGHIRQETVGTLDD    | 246 | prot      |
| 50  | DGSVSIIMDGSYEGILAWVTVNFLTGTQLHGRQETVGTLDD       | 246 | mut npase |
| 201 | GGASTQITFLPQFEKTEQTPRGYLTSEEMFNSTYKLYTH         | 246 | prot      |
| 200 | GGASTQITFLPQFEKTEQTPRGYLTSEEMFNSTFKLYTH         | 246 | mut npase |
| 241 | SYLGFGLKAAPLATLGALSETEGTDGHTERSACLPRWLEAE       | 246 | prot      |
| 240 | SYLGFGLKAAPLATLGALFAKIGTDGHTERSACLPRWLEAE       | 246 | mut npase |
| 281 | WIFGGVKYQYGGNQEGERVGFEPACYAEVLRVVRIGKLHQPEE     | 246 | prot      |
| 280 | WIFGGVKYQYGGNQEGERVGFEPACYAEVLRVVOGKLHQPEE      | 246 | mut npase |
| 321 | VQRGSFYAFSYYYYDRAVIDTDMIDYEKGGILKVEDFERKAR      | 246 | prot      |
| 320 | VRGSFYAFSYYYYDRAADTHILIDYEKGGVLKVEDFERKAR       | 246 | mut npase |
| 361 | EVCDNLSEINFSGSPFLCMDSLTYITALLKDGEGLGFAADSTVLIQ  | 246 | prot      |
| 360 | EVCDNLGSFSGSPFLCMDLTYITALLKDGLGFAERHPIT         | 246 | mut npase |
| 401 | ETKKVNNIETGW-ALGADF-----HELLOS LGISH            | 246 | prot      |
| 400 | -BHKSESEQHRDWLGLGGHILSEAPVSGHHQURPSSTSEACI      | 246 | mut npase |
| 428 |   | 246 | prot      |
| 439 | SEPVESESQEGVDSSETESDLSGKAWPECB                  | 246 | mut npase |

Figure 4

# Apyrase Conserved Regions in CD39-L4



|         |                |   |       |   |   |       |   |      |   |           |   |   |           |
|---------|----------------|---|-------|---|---|-------|---|------|---|-----------|---|---|-----------|
| ACR I   | CD39-L4        | <table border="1"> <tr><td>F</td></tr> <tr><td>L</td></tr> <tr><td>L</td></tr> </table> | F     | L   | L | DAGST | <table border="1"> <tr><td>G</td></tr> <tr><td>H</td></tr> <tr><td>H</td></tr> </table> | G    | H | H         | T | R | I         |
| F       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| L       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| L       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| G       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| H       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| H       |                |   |       |   |   |       |   |      |   |           |   |   |           |
|         | CD39-L4 mutant |   | DAGST | <table border="1"> <tr><td>H</td></tr> <tr><td>T</td></tr> <tr><td>T</td></tr> </table> | H | T     | T   | S    | I |           |   |   |           |
| H       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| T       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| T       |                |   |       |   |   |       |   |      |   |           |   |   |           |
|         | CD39           |   | DAGSS | <table border="1"> <tr><td>H</td></tr> <tr><td>T</td></tr> <tr><td>S</td></tr> </table> | H | T     | S   | S    | L |           |   |   |           |
| H       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| T       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| S       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| ACR II  | CD39-L4        | <table border="1"> <tr><td>P</td></tr> <tr><td>V</td></tr> <tr><td>V</td></tr> </table> | P     | V   | V | PV    | <table border="1"> <tr><td>V</td></tr> <tr><td>Y</td></tr> <tr><td>Y</td></tr> </table> | V    | Y | Y         | L | K | ATAGILRLL |
| P       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| V       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| V       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| V       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| Y       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| Y       |                |   |       |   |   |       |   |      |   |           |   |   |           |
|         | CD39-L4 mut    |   | PV    | <table border="1"> <tr><td>Y</td></tr> <tr><td>Y</td></tr> <tr><td>Y</td></tr> </table> | Y | Y     | Y   | L    | G | ATAGIIRLL |   |   |           |
| Y       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| Y       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| Y       |                |   |       |   |   |       |   |      |   |           |   |   |           |
|         | CD39           |   | PV    | <table border="1"> <tr><td>Y</td></tr> <tr><td>Y</td></tr> <tr><td>Y</td></tr> </table> | Y | Y     | Y   | L    | G | ATAGMRLL  |   |   |           |
| Y       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| Y       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| Y       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| ACR III | CD39-L4        | <table border="1"> <tr><td>M</td></tr> <tr><td>E</td></tr> <tr><td>M</td></tr> </table> | M     | E   | M | M     | <table border="1"> <tr><td>E</td></tr> <tr><td>T</td></tr> <tr><td>M</td></tr> </table> | E    | T | M         | C | S | DEGI      |
| M       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| E       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| M       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| E       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| T       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| M       |                |   |       |   |   |       |   |      |   |           |   |   |           |
|         | CD39-L4 mut    |   | M     | <table border="1"> <tr><td>T</td></tr> <tr><td>T</td></tr> <tr><td>T</td></tr> </table> | T | T     | T   | E    | Q | DEGI      |   |   |           |
| T       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| T       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| T       |                |   |       |   |   |       |   |      |   |           |   |   |           |
|         | CD39           |   | T     | <table border="1"> <tr><td>L</td></tr> <tr><td>L</td></tr> <tr><td>L</td></tr> </table> | L | L     | L   | EEGA | Y | GWITIN    |   |   |           |
| L       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| L       |                |   |       |   |   |       |   |      |   |           |   |   |           |
| L       |                |   |       |   |   |       |   |      |   |           |   |   |           |

**FIG. 5**

Nucleotide sequence of the CD39-L4 mutant ACRIII (SEQ ID NO:6). The nucleotide changes have been highlighted. The G to A and A to C changes at positions 502 and 503 produce a Thr, the T to C, C to A and C to A changes at positions 508-510 result in a Gln and the A to C changed at position 525 result in a Phe.

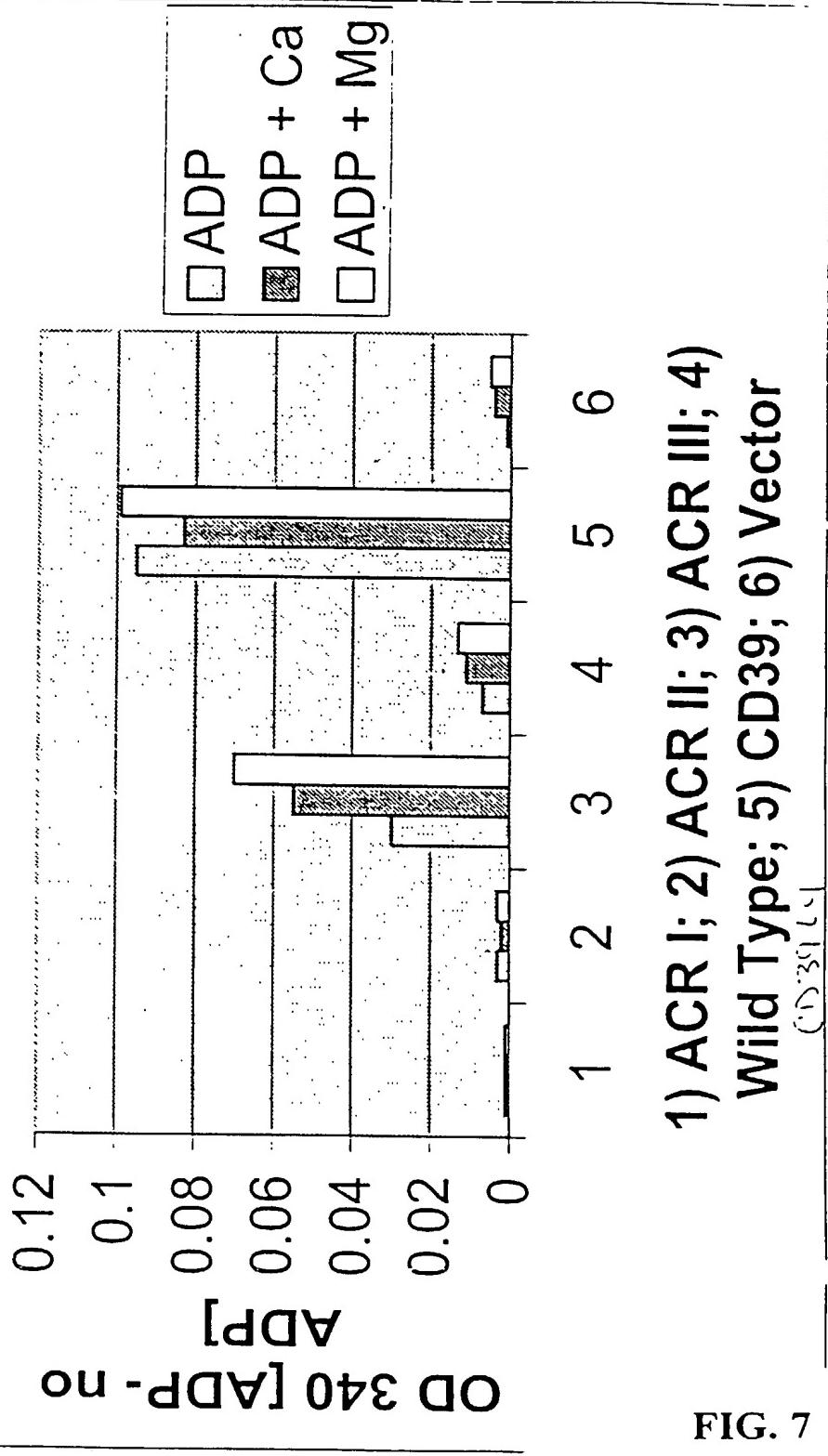
ATGGCCACTTCTGGGGCACAGTC~~T~~GGTGGTATCCTGT~~T~~TGCAGCGCTGTCT  
CCCACAGGAACCAGCAGACTTGGTTTGAGGGTATCTTCTGTCTTCCATGTGCCCATCAATGT  
CAGCGCCAGCACCTGTATGAAATTATGTTGATGCAGGGAGCACTGGA~~A~~CTGAATTATGTT  
TACACCTTGTGCAGAAAATGCCAGGACAGCTTCAATTCTAGAAGGGGAAGTTTGATTCTG  
TGAAGCCAGGACTTTCTGCTTTGTAGATCAACCTAACGAGGGTGCTGAGACC~~G~~TCAAGGGCT  
CTTAGAGGTGGCAAAGACTCAATCCCCGAAGTCACTG~~G~~AAAAAGACCCAGTGGTCTAAAG  
GCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCAAGGCTCTGCTTTGAGGTAAGG  
AGATCTTCAGGAAGTCACCTTCTGGTACCAAAGGGCAGTGT~~T~~AGCATCATGACTGGACAAGA  
CGAAGGCATATT~~C~~GCTTGGGTACTGTGAATTCTGACAGGT~~C~~AGCTGCATGGCCACAGACAG  
GAGACTGTGGGGACCTTGGACCTAGGGGAGCCTCACCCAAATCACGTTCTGCCCCAGTTG  
AGAAA~~A~~CTCTGGAACAAACTCCTAGGGCTACCTCACTTCTTGAGATGTTAACAGCACTTA  
TAAGCTCTATAACACATAGTTACCTGGGATTGGATTGAAAGCTGCAAGACTAGCAACCC~~T~~GGGA  
GCCCTGGAGACAGAAGGGACTGATGGGACACTTCCGGAGTGCCTGTTACCGAGATGGT~~T~~GG  
AAGCAGAGTGGATCTTGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAAGGGAGGTGGG  
CTTGAGCCCTGCTATGCCGAAGTGT~~G~~AGGGTGGTACGAGGAAAAC~~T~~TCACCAGCCAGAGGAG  
GTCCAGAGAGGTTCTTCTATGCTTTCTTACTATTATGACCGAGCTGT~~G~~ACACAGACATGA  
TTGATTATGAAAAGGGGGTATTAAAGTTGAAGATTTGAAAGAAAAGCCAGGGAAAGTGTG  
TGATAACTTGGAAAAC~~T~~TCACC TCAGGCAGTCCCTTCTGTGCATGGATCTCAGCTACATCAC  
AGCCCTGTTA AAGGATGGCTTGGCTTGCAAGACAGCACAGTCTACAGCTCACAAAGAAAGT  
GAAC AACATAG AGACGGGCTGGGCCTGGGGGCCACCTTCACCTGT~~T~~GCAGTCTGGCA  
TCTCCCATTGA

Amino acid sequence of CD39-L4 mutant ACR III (SEQ ID NO:7). The amino acid changes are D to T (a.a. 168), S to Q (a.a. 170) and L to F (a.a. 175). The changes are shown in bold.

MATSYGTVF~~F~~MLVVSCVCSAVSHRNQQTWFEGIFLSSMCPINV~~S~~ASTLYGIMFDAGSTGT  
RIHVYT~~F~~VQKMPGQLPILEGEVFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW  
KKTPVVLKATAGLRLP~~E~~HKA~~K~~ALLFEVKEIFRKSPFLVPKG~~S~~V~~I~~MTGQDEGI~~P~~AWVTV  
NFLTGQLHGH~~R~~QETVGTLDLG~~G~~ASTQITFLPQF~~E~~KTLEQ~~T~~PRGYLT~~S~~FEMFN~~Y~~KLYTH  
SYLG~~F~~GLKAARLATLGA~~E~~TEGTDGHTFRSACLPRWLEAEWIFGGV~~K~~YQYGGNQE~~G~~EVGF  
EPCYAEVLRVVRGKLHQPEEVQRGSFYAFS~~Y~~YDRAVDTDMIDYE~~K~~GGILKVEDFERKAR  
EVCDNLENFTSGSPFLCMDLSY~~I~~TALLKDGF~~G~~FADSTV~~L~~QLTKVNNIETGWALGATFHL  
LQSLGISH

FIG. 6

## FIG. 2 ADPase activity of CD39-L4 ACR mutants



Atty Docket No. 28110/35908  
 Serial No.: 09/370,265  
 Title: Methods and Materials Relating to Novel  
 CD39-Like Polypeptides

Figure 8

|               |   |                    |   |     |
|---------------|---|--------------------|---|-----|
| SEQ ID No-3   | MAT SWG   | - - - - -          | V F F M L V V S C V C S A V S H R N Q Q T W F E G I F L S S M C P I N V S A S     | 46  |
| SEQ ID No-5   | MAT SWGT  | - - - - -          | - V F F M L V V S C V C S A V S H R N Q O O T W F E G I F L S S M C P I N V S A S | 46  |
| CD39Human.seq | MEDTKESNVKTFC SK NILA I L G F S S I A V I A - - - - -   | LLAVGLTQ - - - - - | N K A L P E N   | 46  |
| SEQ ID No-3   | TLY G I M F D A G S T G T R I H V Y T F V Q K M P G Q L P I L E G E V F D S V K                                     | - - - - -          | P G L S A F V D Q P K Q G   | 100 |
| SEQ ID No-5   | TLY G I M F D A G S T G T R I H V Y T F V Q K M P G Q L P I L E G E V F D S V K                                     | - - - - -          | P G L S A F V D Q P K Q G   | 100 |
| CD39Human.seq | V K I Y G I V L D A G S S H T S S L Y I Y K W P A E K E N D T G V V H Q V E E C R V N K G P G I S K F V Q K V N E I | 101                | 101   | 101 |
| SEQ ID No-3   | A E T V Q G I L L E V A K D S I P R S H W K K T P V V L K A T A G L R L L   | - - - - -          | P E H K A K A L L F E V K E I F   | 152 |
| SEQ ID No-5   | A E T V Q G I L L E V A K D S I P R S H W K K T P V V L K A T A G L R L L   | - - - - -          | P E H K A K A L L F E V K E I F   | 152 |
| CD39Human.seq | G I Y L T D C M E R A R E V I P R S Q H Q E T P V Y L G A T A G M R L L   | 152                | 152   | 152 |
| SEQ ID No-3   | R K S P F L V P K G S V S I M D G S D E C I L A W V T V N F L T G Q L   | - - - - -          | - - - - -   | 195 |
| SEQ ID No-5   | R K S P F L V P K G S V S I M D G S D E C I L A W V T V N F L T G Q L   | - - - - -          | - - - - -   | 195 |
| CD39Human.seq | S N Y P F D F Q - - G A R I I T G Q E G A Y C W I T I N Y L L G K F S Q K T R W F S I V P Y E T N N Q E T F         | 195                | 195   | 195 |
| SEQ ID No-3   | G T L D L G G A S T Q I T F L P Q F E K T L E Q T P R G Y L T S F E M F N S T Y K L Y T H S Y L G F G L K A A       | - - - - -          | - - - - -   | 250 |
| SEQ ID No-5   | G T L D L G G A S T Q I T F L P Q F E K T L E Q T P R G Y L T S F E M F N S T Y K L Y T H S Y L G F G L K A A       | - - - - -          | - - - - -   | 250 |
| CD39Human.seq | G A L D L G G A S T Q I T F L P Q F E K T L E Q T P R G Y L T S F E M F N S T Y K L Y T H S Y L G F G L K A A       | 250                | 250   | 250 |
| SEQ ID No-3   | - - R L A T L G A L E T E G - - -   | - - - - -          | - - - - -   | 261 |
| SEQ ID No-5   | - - R L A T L G A L E T E G - - -   | - - - - -          | - - - - -   | 261 |
| CD39Human.seq | L W Q K L A K D I Q V A S N E I L R D P C F H P G Y K K V V N V S D L Y K T P C T K R - F E M T L P E Q Q F -       | 261                | 261   | 261 |
| SEQ ID No-3   | Y Q Y G G N Q E G E V G F E P C Y A E V L R V V R G K   | - - - - -          | T D G H T F R S A C L P R W L E A E W I F G G V K                                 | 287 |
| SEQ ID No-5   | Y Q Y G G N Q E G E V G F E P C Y A E V L R V V R G K   | - - - - -          | T D G H T F R S A C L P R W L E A E W I F G G V K                                 | 287 |
| CD39Human.seq | - - - E I Q G I G N Y Q Q C H Q S T I L E L F N T S Y C P Y S Q C A F N G I F L P P L Q G D F G A E S [A] F -       | 287                | 287   | 287 |
| SEQ ID No-3   | Y Y Y D R - - A V D T D M I D Y E K G G I L K V E D F E R K A R E V C D N L E N F T S G S P - F L - - - C M         | 330                | 330   | 330 |
| SEQ ID No-5   | Y Y Y D R - - A V D T D M I D Y E K G G I L K V E D F E R K A R E V C D N L E N F T S G S P - F L - - - C M         | 330                | 330   | 330 |
| CD39Human.seq | - Y F V M K F L N I T S E K V S Q E N V T E M - M K K E C A Q P W E - - E I K T S Y A G V V K E K Y [L] S E Y [C] F | 363                | 363   | 363 |
| SEQ ID No-3   | D L S Y I T A L L K D G F G F A D S T - - - - -   | - - - - -          | V L Q L T K K V N N I E T G W   | 412 |
| SEQ ID No-5   | D L S Y I T A L L K D G F G F A D S T - - - - -   | - - - - -          | V L Q L A A - - - - -   | 402 |
| CD39Human.seq | - Y F V M K F L N I T S E K V S Q E N V T E M - M K K E C A Q P W E - - E I K T S Y A G V V K E K Y [L] S E Y [C] F | 412                | 412   | 412 |
| SEQ ID No-3   | D L S Y I T A L L K D G F G F A D S T - - - - -   | - - - - -          | V L Q L T K K V N N I E T G W   | 459 |
| SEQ ID No-5   | D L S Y I T A L L K D G F G F A D S T - - - - -   | - - - - -          | V L Q L A A - - - - -   | 459 |
| CD39Human.seq | - Y F V M K F L N I T S E K V S Q E N V T E M - M K K E C A Q P W E - - E I K T S Y A G V V K E K Y [L] S E Y [C] F | 459                | 459   | 459 |
| SEQ ID No-3   | A L G A T F H L L Q S L G I S H   | - - - - -          | - - - - -   | 428 |
| SEQ ID No-5   | - - - - -   | - - - - -          | - V L R - - - - -   | 406 |
| CD39Human.seq | - N M I P A E Q P P L S T P L S H S T Y V F L M V L F S L V L F T V A I I G L L I F H P                             | 406                | 406   | 406 |

FIG 8

mur ntpase MAT SWGA -MLIIACV[G]ST[V]FYREQQTWFEGVFLLSSMCPINV' S[T]FYCIMFDA 54  
SEQ ID No-3 MAT SWG1 'FM LVVSCVC SAVSHRNQQTWFEGIFFLSSSMCPINV' .S[TLYCIMFDA 55  
SEQ ID No-5 MAT SWGTV FFM LVVSCVC SAVSHRNQQTWFEGIFFLSSSMCPINV SASTLYCIMFDA 55

mur ntpase GST GTRIH VYT FV QK [T]AG QL P[E]LEG E IFDSV KPG LSAF VDQ P KQGA ET VQ [EL]EV 109  
SEQ ID No-3 GST GTRIH VYT FV QK M P G Q L P ILE G E VFD SV KPG LSAF VDQ P KQGA ET VQ G L L E V 110  
SEQ ID No-5 GST GTRIH VYT FV QK M P G Q L P ILE G E VFD SV KPG LSAF VDQ P KQGA ET VQ G L L E V 110

mur ntpase AK DS I PR SHW E RT P V V L K A TAG L R L L P E Q K A Q A L L L E V E E I F K N S P F L V P [DGSVS 164  
SEQ ID No-3 AK DS I PR SHW K K T P V V L K A TAG L R L L P E H K A K A L L F E V K E I F R K S P F L V P K G S V S 165  
SEQ ID No-5 AK DS I PR SHW K K T P V V L K A TAG L R L L P E H K A K A L L F E V K E I F R K S P F L V P K G S V S 165

mur ntpase IMD GS Y E G I L A W V T V N F L T G Q L H C R G Q E T V G T L D L G G A S T Q I T F L P Q F E K T L E Q T 219  
SEQ ID No-3 IMD GS D E G I L A W V T V N F L T G Q L H C H R Q E T V G T L D L G G A S T Q I T F L P Q F E K T L E Q T 220  
SEQ ID No-5 IMD GS D E G I L A W V T V N F L T G Q L H C H R Q E T V G T L D L G G A S T Q I T F L P Q F E K T L E Q T 220

mur ntpase PR GYL TS F E M F N S T E K LY T H S Y L G F G L K A A R L A T L G A L E A K G T D G H T F R S A C L P R 274  
SEQ ID No-3 PR GYL TS F E M F N S T Y K LY T H S Y L G F G L K A A R L A T L G A L E T E G T D G H T F R S A C L P R 275  
SEQ ID No-5 PR GYL TS F E M F N S T Y K LY T H S Y L G F G L K A A R L A T L G A L E T E G T D G H T F R S A C L P R 275

mur ntpase W L E A E W I F G G V K Y Q Y G G N Q E G E M G F E P C Y A E V L R V V Q [G K L H Q P E E V R G S A F Y A F S 329  
SEQ ID No-3 W L E A E W I F G G V K Y Q Y G G N Q E G E M G F E P C Y A E V L R V V R G K L H Q P E E V V Q R G S F Y A F S 330  
SEQ ID No-5 W L E A E W I F G G V K Y Q Y G G N Q E G E M G F E P C Y A E V L R V V R G K L H Q P E E V V Q R G S F Y A F S 330

mur ntpase YY Y D R A A D T H L I D Y E K G G V L K V E D F E R K A R E V C D N L G S F S S G S P F L C M D L T Y I T A 384  
SEQ ID No-3 YY Y D R A V D T D M I D Y E K G G I L K V E D F E R K A R E V C D N L E N F T S G S P F L C M D L S Y I T A 385  
SEQ ID No-5 YY Y D R A V D T D M I D Y E K G G I L K V E D F E R K A R E V C D N L E N F T S G S P F L C M D L S Y I T A 385

mur ntpase LL K D G L C F A E R H P [LT - A H R E S E Q H R D W L G L G H L S P A P V S G H H Q L R P S S T S E A C I 438  
SEQ ID No-3 LL K D G F G F A D S T V L Q [LT K K V N N I E T G W - A L G A T F - - - - - H L L Q S L G I S - - - - - 427  
SEQ ID No-5 LL K D G F G F A D S T V L Q - A - 405

mur ntpase SEP V F S Q E G V D S E T F S D L S G K A W P E T R 465  
SEQ ID No-3 - 428  
SEQ ID No-5 - 406

FIG 9